

FIGURE 1

SEQ ID NO: 1

>STAAU_R009 nucleotide sequence: 1800
TTGCCAATAGATCAATCGATCATTAATGAAATAAAAGATAAAACCGACATTTTAGACTTGGTAAGTGAATATGTAAATTAGAAAAGAG
AGGACGCAATTATATAGGTTTGTGTCCTTTTCATGATGAAAAGACACCTTCATTTACAGTTTCTGAAGATAAACAAATTTGTTCATTGTT
TTGGTTGTAATAAGGTGGCAATGTTTCAATTTACTCAAGAAATTAAGACATATCATTTGTTGAAGCGGTTAAAGAAATTAGGTGAT
AGAGTTAATGTTGCTGTAGATATTGAGGCAACACAACTCTAACTCAAATGTTCAAATGCTTCTGATGATTTACAAATGATTGAAATGCA
TGAGTTAATACAAGAAATTTATTATTACGCTTTAACAAGACAGTCGAAGCGCAACAGCATTAACGTACTTACAAGAACGTTGTTTA
CAGATGCGCTTATTAAAGAGCGAGGCATTGGCTTTGCCCCGATAGCTCACATTTTGTGTCATGATTTTCTTCAAAAAAAGGTTACGAT
ATTGAATTAGCATATGAAGCCGGATTATTATCACGTAAACGAAGAAAATTTTCAGTTATTACGATAGATTTTCGAAATCGTATTATGTTTCC
TTTGAAAAATGCGCAAGGAAGAAATTTGTTGGATATTTCAGGTCGAACATATACCGGTCAAGAACCAAAATACTTAAATAGTCTGAAACAC
CTATCTTTCAAAAAAAGAAAGTTGTTATACAACTTAGATAAAGCGGTAATCAATTAGAAAAATTAGATGAAATCGTATTACTAGAAAGGT
TTTATGGATGTTATAAAATCTGATACCTGCTGGCTTGAAAAACGTTGTTGCAACAATGGGTACACAGTTGTCAGATGAACATATTACTTT
TATACGAAAGTTAACATCAAAATATAACATTAATGTTTGTATGATGGGATTTTGCAGGTAGTGAAGCAACACTTAAAAACAGGTCAAAATTTGT
TACAGCAAGGGCTAAATGTATTGTTATACAAATTGCCATCAGGCATGGATCCGGATGAATACATTTGTAAGTATGGCAACGATGCAATTT
ACTGCTTTTGTAAAAAATGACAAAAAGTCATTTGCACATTATAAAGTGAGTATATAAAGATGAAATGACATATGACCTTTTCATA
TGAACGTTATTGAAAGAACTAAGTCATGATATTTCGCTTATGAAATCATCGATTTTGCACAAAGGCTTTAAATGATGTTGCACCAT
TTTTCAATGTTAGTCCTGAGCAATTAGCTAACGAAATACAATTCAAATCAAGCACCCAGCCAATTAATTATCCAGAAAGATGAGTATGGCGGT
TACATTGAAACCTGAGCCAAATTGGTATGGCACAATTTGACAATTTGAGCCGTCAGAAAAAGCGGAGCGAGCATTTTAAACATTTAAAT
GAGAGATAAAGATACATTTTAAATTTATGAAAGTGTGATAAGGATAACTTCACAAATCAGCATTTTAAATATGTTATTCGAAGTCT
TACATGATTTTATGCGGAAATGATCAATATAATATCAGTGATGCTGTGAGTATGTTAATTCAAATGAGTTGAGAGAAACACTAAT
AGCTTAGAACCAATATAATTTGAATGACGAACCATATGAAAAATGAAATTTGATGATTATGTCAAATGTTTATTAATGAAAAAGGACAAAGAAC
AATTGAGTCATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTAGAATTACAAAAATACTATTACAGCAAAATTTGTTGCTA
AGAATAAAGAACCGCATGTAG

TCF "SECRET"

SEQ ID NO: 2

>STAAU_R009 amino acid sequence : 599
LRIDQSIINEIKDKTDILDVSEYVKLEKGRNYYIGLCPFHDEKTPSFTVSEDKQICHCFGCKKGGNVFQFTQEIKDISFVEAVKELGD
RVNVAVDIEATQSNVQIASDDQLQMIEMHELIIQEFYYALTKTVEGEQALTYLQERGFTDALIKERGIGFAPDSSHFCHDFLQKKGYD
IELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRITYTGQEPKYLNSPETPIFQKRKLLYNLDKARKSIRKLDEIVLLEG
FMDVIKSDTAGLKNVVATMGTOQSDEHITFIRKLTSTNITLMFDGDFAGSEATLKTGQNLQQLNVFVIQLPSGMDPDEYIGKYGNDAF
TAFVKNDDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVSPQLANEIQFNQAPANYYPEDEYGG
YIEPEPIGMAQFDNLSRQEKAEAFKHLMRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI
SLEQYNLNDEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIVAKNKERM

FIGURE 2

SEQ ID NO: 3

>96ORF078 nucleotide sequence
ATGAATATAATGCAATTCAAAAGCTTATTGAAATCGATGTATGAAGAGACAAAGCAAAGC
GACCCGATTGTAGCAAATGTATATCGAGACTGGTTGGCGGTCAATAGATTGTTGGAC
AATAACGAGTTATCGCCCTTTCGATGATTACGACAGAGTTGAAAAGAAAATCATGAATGAA
ATCAACTGGAAGAAACACACATTAAGGAGTGTAA

SEQ ID NO: 4

>96ORF078 amino acid sequence 96_NT|10148-10363|
MNIMQFKSLLKSMYEETKQSDPIVANVYIETGWAVNRLLDNNELSPFDDYDRVEKKIMNE
INWKKTHKEC

FIGURE 3

A.

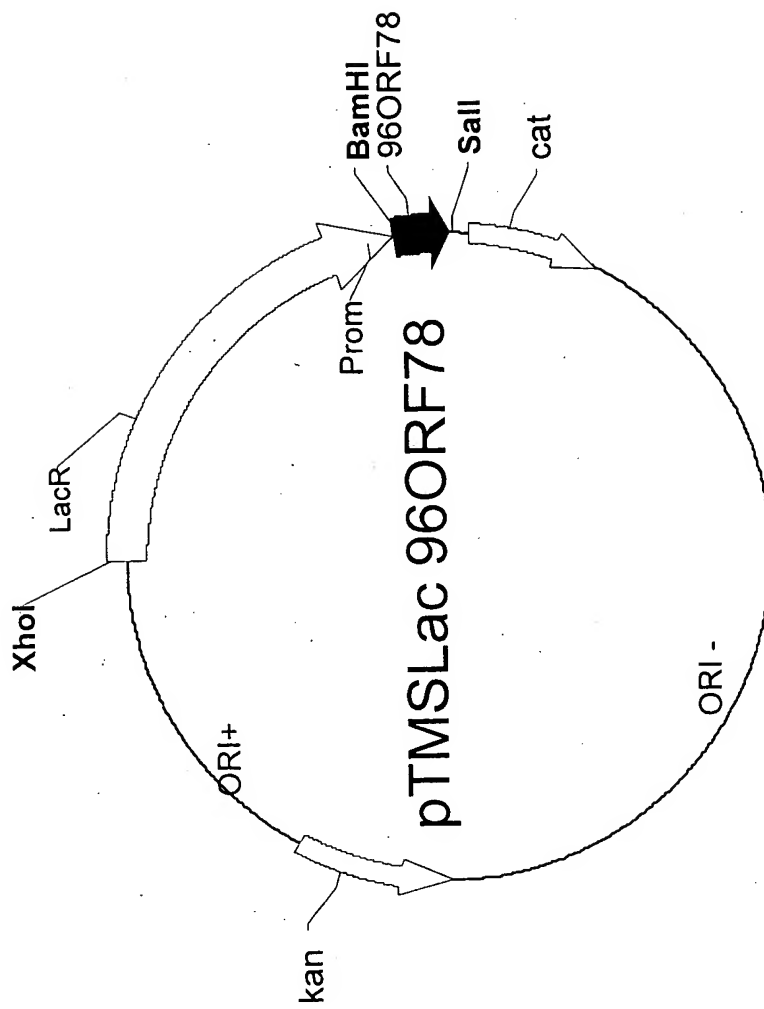


FIGURE 3 B.

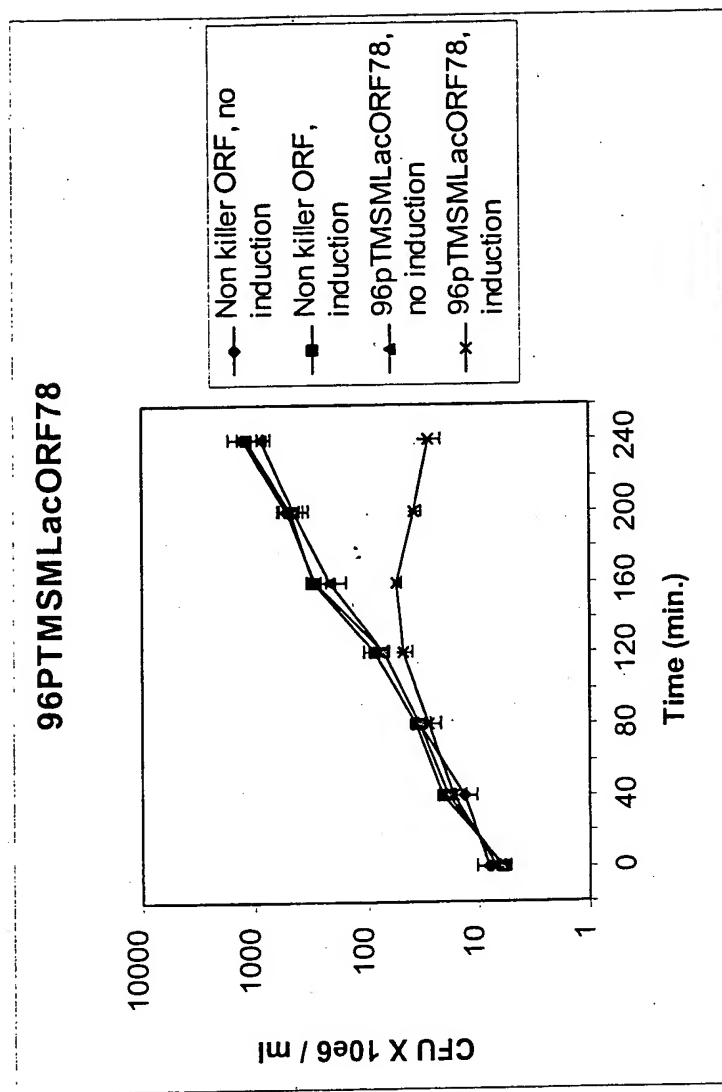
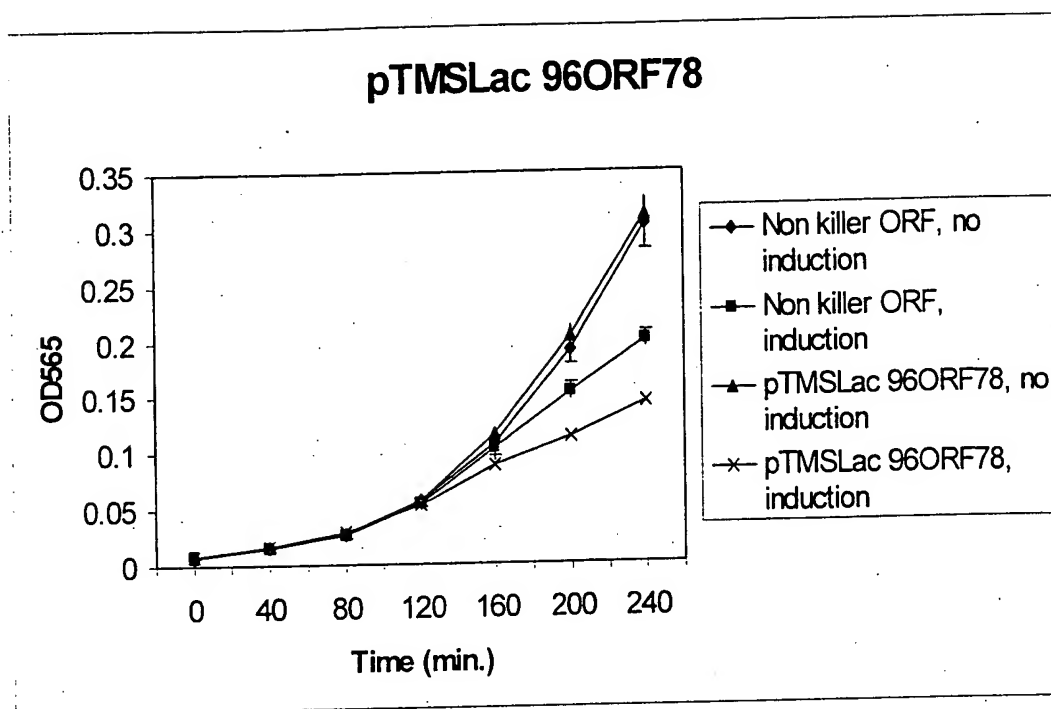


FIGURE 3 C.



D.

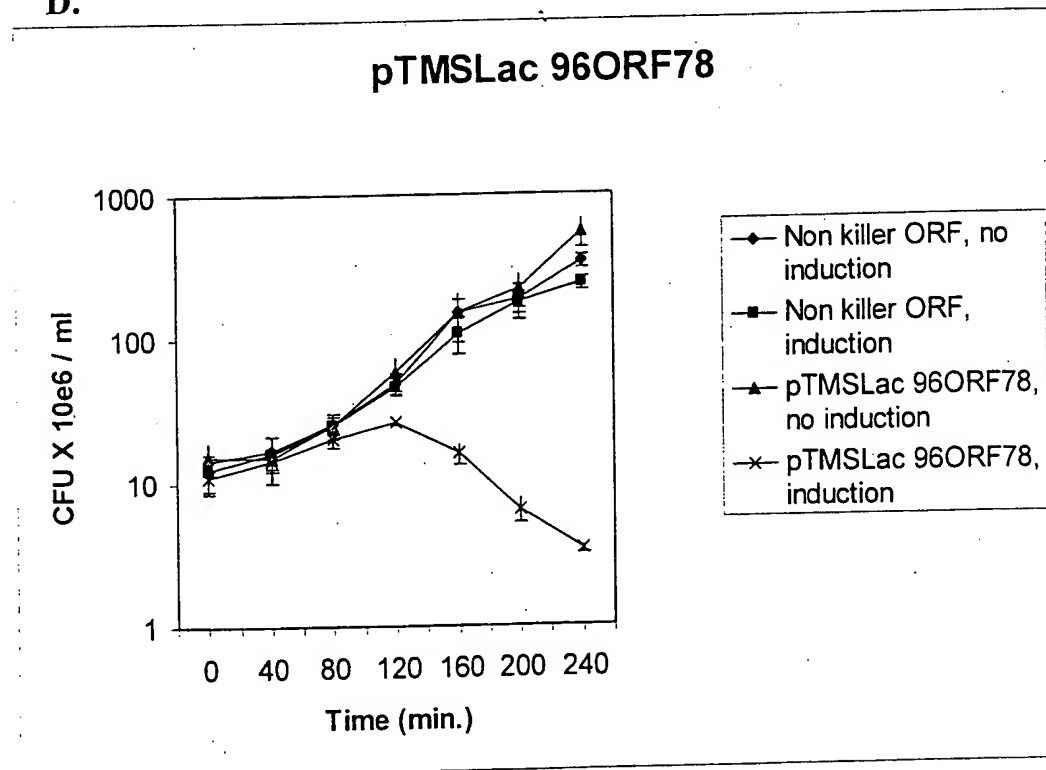
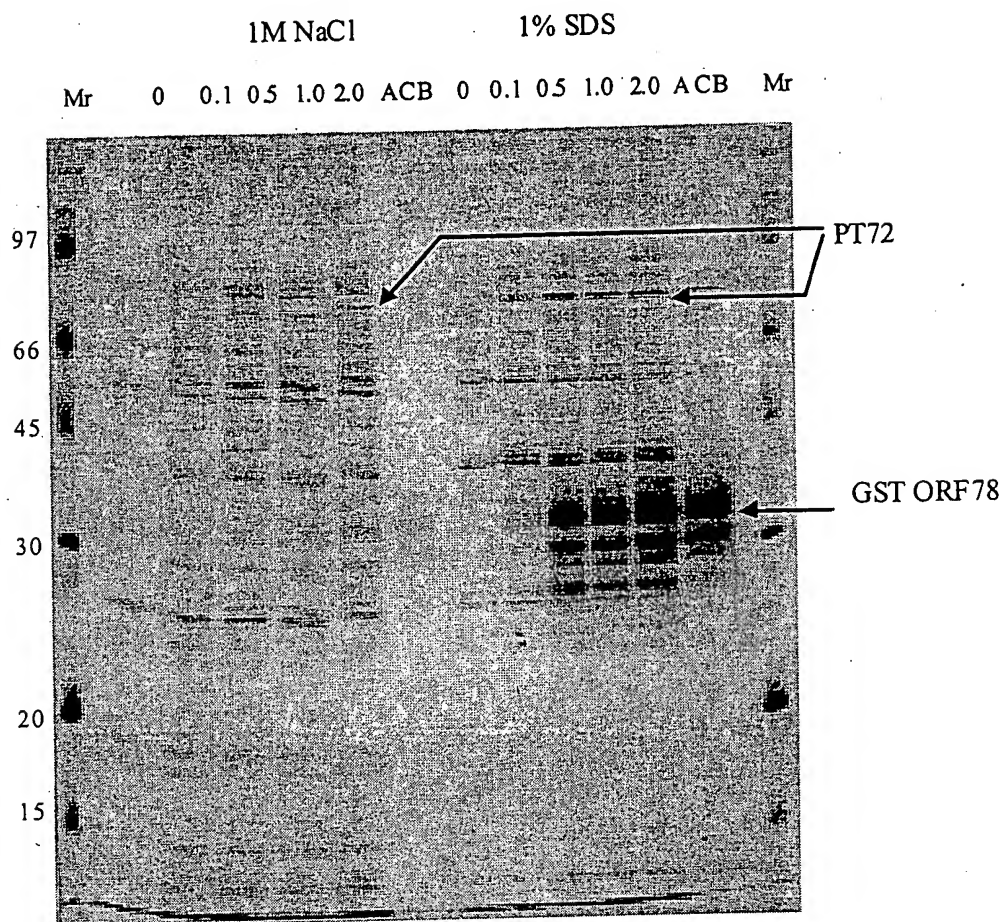


FIGURE 4

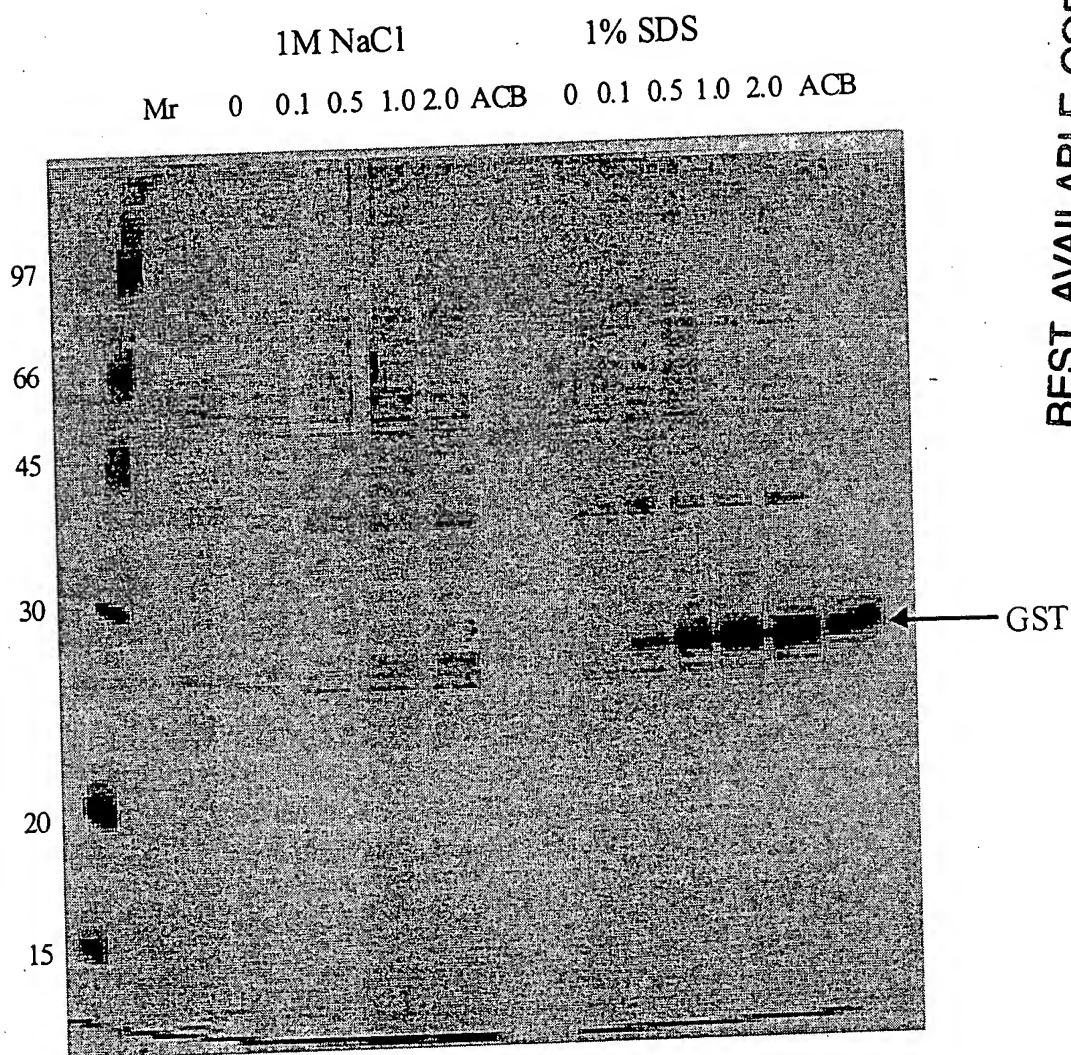
A. GST/96ORF78



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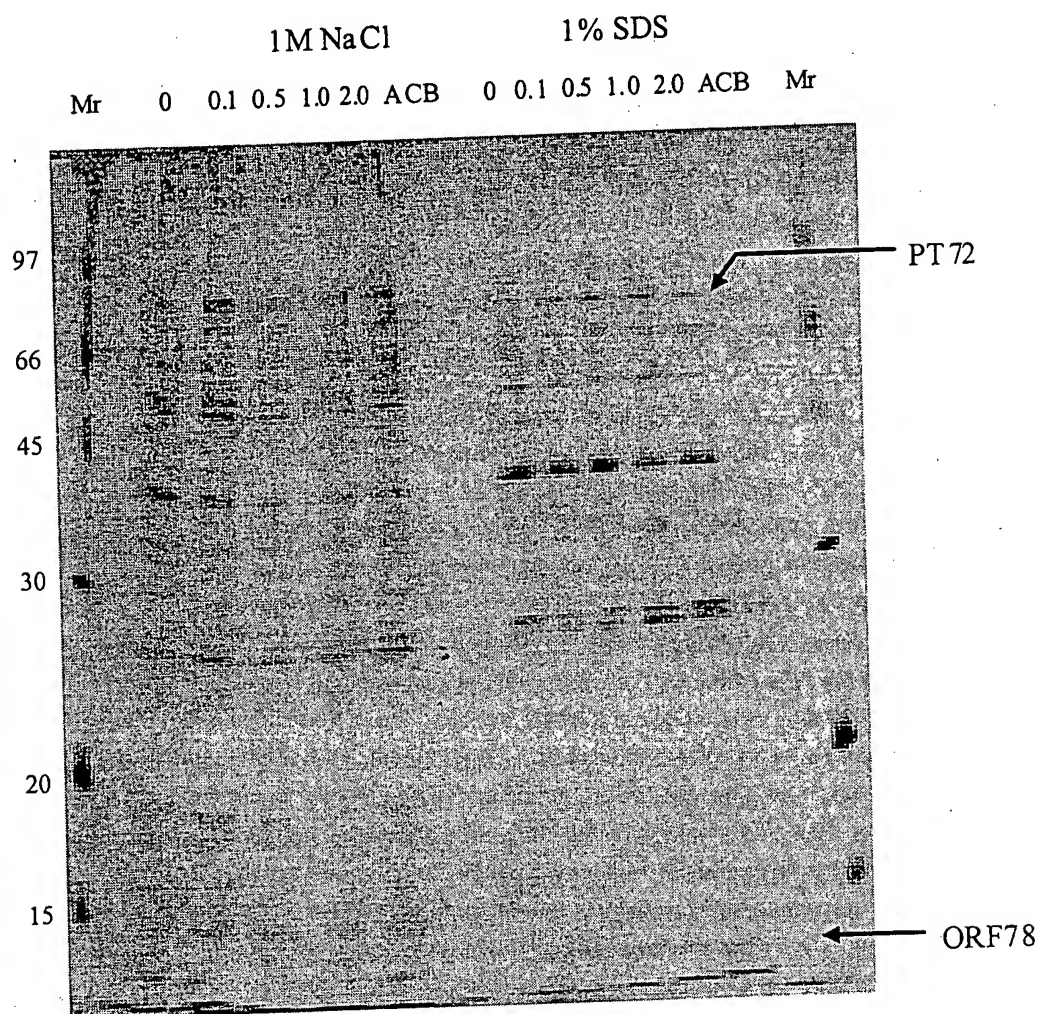
FIGURE 4

B. GST



BEST AVAILABLE COPY

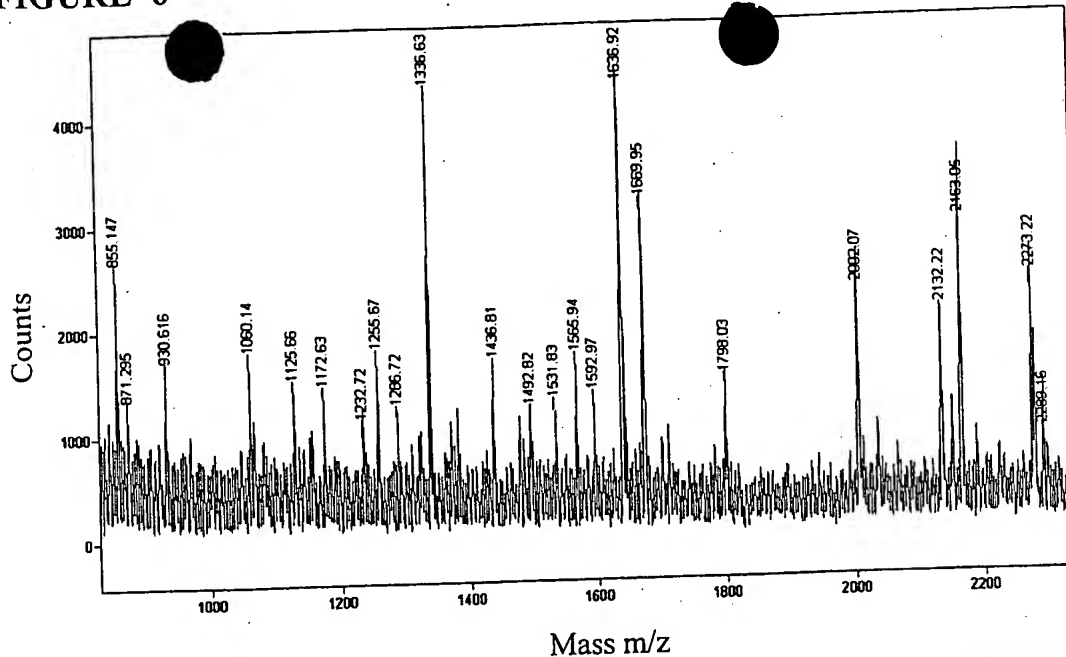
FIGURE 5 96ORF78 (GST removed)



1005221 2252001

TEST AVAILABLE COPY

FIGURE 6



TOGETHER "22252001"

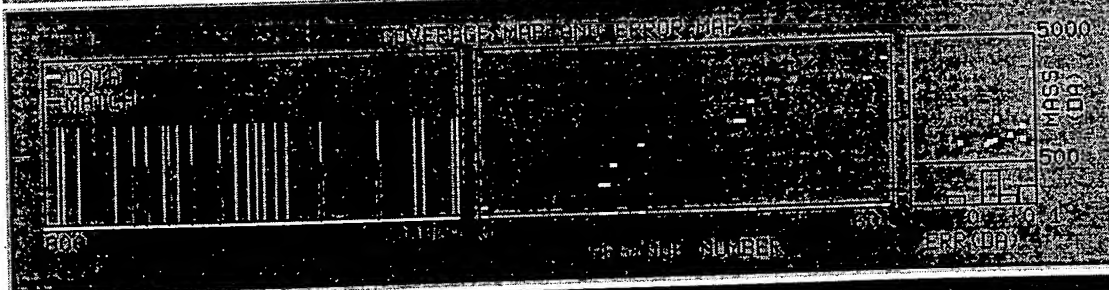
ouContig286: 82020 to 83822: Frame 3 601 aa

Sample ID : orf78 72 [Pass:0]

Measured peptides : 23

Matched peptides : 7

Min. sequence coverage: 14%



1124.649	M	1124.622	0.027	588	596	0	YYEQIVAK
1171.623	M	1171.590	0.033	394	403	0	ELSHDISLMK
1171.623	M	1171.644	0.021	5	14	0	IDQSINEIK
1254.661	M	1254.620	0.041	563	573	0	GOETIESLNHK
1335.627	M	1335.536	0.091	193	202	0	NEENESYDR
1435.802	M	1435.734	0.068	233	244	0	YLNSPETPIFOK
1797.019	M	1796.930	0.089	177	192	1	KGYDIELAYEAGLLSR
2001.060	M	2001.016	0.044	374	390	1	VSILKDEIAHNDLSYER

855.147 871.295 930.616 1060.140 1232.717 1286.716 1492.822 1531.830 1565.943 1592.967
1636.921 1669.948 2132.217 2163.048 2273.222 2289.164

FIGURE 7A

A. Pfam HMM search results

Model	Seq-from	Seq-to	HMM-from	HMM-to	Score	E-value
zf-CHC2	3	100	1	98	198.4	1.1e-55
Toprim	260	339	1	151	71.9	1.3e-17

Alignments of top-scoring domains:

zf-CHC2:
domain 1 of 1, from 3 to 100: score 198.4, E = 1.1e-55
*->ipeesIdelknriDIVdvisYvKkGrnYkgLCPFHdEKTSPFs
i++++I+e+k++++DI d++seYvKL+K+GrnY+gLCPFHdEKTSPF+
gi|133988 3 IDQSIINEIKDKTDILDVSEYVVKLEKGRNYIGLCPFHdEKTSPFT 49

gi|133988 50 VSEDKQICHCFGCKKGGNVFQFTQEIKDIDISFVEAVKELGDRVNVAVDIEA 99

g<-*
+
gi|133988 100 T 100

TOPPRIM "22222222"

Toprim: domain 1 of 1, from 260 to 339: score 71.9, E = 1.3e-17

*->kvliiVEgpsdakalagkpskrkivyelpggkdgnvvaslGhlv
 +nvva++G+
 +++++ Eg++d+++ a+
 DEIVLLEGFMVDVIKSDTAGL-----KNVVATMGQTQ- 289

gi|133988 260 dLptpegyddkykwlwlpivdvkkgfepyqiefdqlckcskkidlkkql
 1++e++
 -----LSDEHI 295

gi|133988 290 kllklakkadevilatDpDreGeaiawkllellkpygpveleddkkvrr
 ++kl+++ + l++D+D +G ++++k + l+ +g +v++
 296 TFIRKLTSN---ITLMFDGDGFAGSEATLKTGQNLLOQGL-----NVFV 335

iflp<-*
 i+lp
 336 IQLP 339

gi|133988 336

FIGURE 7B

B. Optimal global alignment of amino acid sequences

Sequence 1 sp|O05338|PRIM_STAAU DNA PRIMASE (EC 2.7.7.-) - S. aureus. (572 letters)

Sequence 2 STAAU_R009 STAAU_R009_NT|1-1800| (599 letters)

Identical: 560/605 (92%), Similar: 564/605 (93%), Gap: 39/605 (6%)

seq1	1	M-----	27
seq2	1	LRIDQSIINEIKDKTDILDVSEYVVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICHCF	60
seq1	28	GCKKGGNVFQFTQEIKDISFVEAVKELGDRNVAVDIEATQSNSNVQIASDDLQMIEMHE	87
seq2	61	GCKKGGNVFQFTQEIKDISFVEAVKELGDRNVAVDIEATQSNSNVQIASDDLQMIEMHE	120
seq1	88	LIQEFYYALTKTVEGEQALTYLQERGTDALIKERGIGFAPDSSHCHDFLQKKGYDIE	147
seq2	121	LIQEFYYALTKTVEGEQALTYLQERGTDALIKERGIGFAPDSSHCHDFLQKKGYDIE	180
seq1	148	LAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIF	207
seq2	181	LAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIF	240
seq1	208	QKRKLLYNLDKARKSIRKLDLDEIVLLEGFMDVIKSDTAGLKNVAVATMGTLSDHEHITFIRK	267
seq2	241	QKRKLLYNLDKARKSIRKLDLDEIVLLEGFMDVIKSDTAGLKNVAVATMGTLSDHEHITFIRK	300
seq1	268	LTSNITLMFDGDFAGSEATLKTGQHLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTTFV	327
seq2	301	LTSNITLMFDGDFAGSEATLKTGQNLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTAFV	360

Foot "22300T"

seq1	328	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKAINDVAPFFNVS	387
seq2	361	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVS	420
seq1	388	PEQLANEIQFNQAPANYYPEDEYGGYDEYGGYIEPEPIGMAQFDNLSRREKAERAFKLHL	447
seq2	421	PEQLANEIQFNQAPANYYPE-----DEYGGYIEPEPIGMAQFDNLSRQEKAEERAFKLHL	474
seq1	448	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLL	507
seq2	475	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLL	534
seq1	508	SLEQYNLNGEPYENEIDDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQQIVAK	567
seq2	535	SLEQYNLNDEPYENEIDDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQQIVAK	594
seq1	568	NKERM	572
seq2	595	NKERM	599

FASTA format

```

seq1 414 APFFNVSPEQLANEIQFNQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKAEAF LKH 473
      | | : | | : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
seq2 415 AEEFSLSLSALHEQLSRQRETKPREAPDGETARP-----MLAKKLLPAFQNAERLLLAH 470

seq1 474 LMRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNIISDAVQYVNSNELRETL 533
      : | | : | | | | : : : | | | | : : : | | | | : : : | | | | : : : | | |
seq2 471 MMRSRDVALVVQERIG-GRFNIEEHRALAAYYIAFYEEGHEADPGALISRI-PGELQPLA 528

seq1 534 ISLEQYNLNDEPYENEIDYV-NVINEKGQETIESLNHKLREATRIGDVELQYYLQQIV 592
      : : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
seq2 529 SDVSLLLIADDVSEQELEDYIRHVLNRPKWLMLKVKEQEKTEAERRKDFLTAARIAKEMI 588

seq1 593 AKNK--ERM 599
      |
seq2 589 EMKKMLSSS 597

```


FOGTE "2223200"

seq1	359	FVKNKKSF	AHKVSIL-KDEIAHNDLSYERYLKELSHDISLMKSSILQOKALNDVAPFF	417
seq2	361	DIIDASVTVM	AFKMQYFRKGNLSDEGDRLAYIKDVLKEISTLSGSLEQEVYVKQLASEF	420
seq1	418	NVSPEQLANEIQFNQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQ-----EKAERAF		470
seq2	421	SLSQESL	TE--QLSVFSKQKPADNSG----ETKTRRAHLTTKARQKRLRPAYENAERLL	474
seq1	471	LKHLMRDKDTFLNYYYESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNELR		530
seq2	475	LAHMLRDRSVIKKVIDRVGFQFNIDEH-RALAAAYLYAFYEEGAELTPQHLMARVTDDHIS		533
seq1	531	ETLISLEQYNLNDEPYENEIDDYV-NVINEKQGETIESLNHKLREATRIGDVELQKYYLQ		589
seq2	534	QLLSDILMLQVNQELSEAELSDYVKKVLNQRNWSMIKEKEAERAEARQKDFLRAASLAQ		593
seq1	590	QIVAKNKERM	599	
seq2	594	EIVTLNRSLK	603	

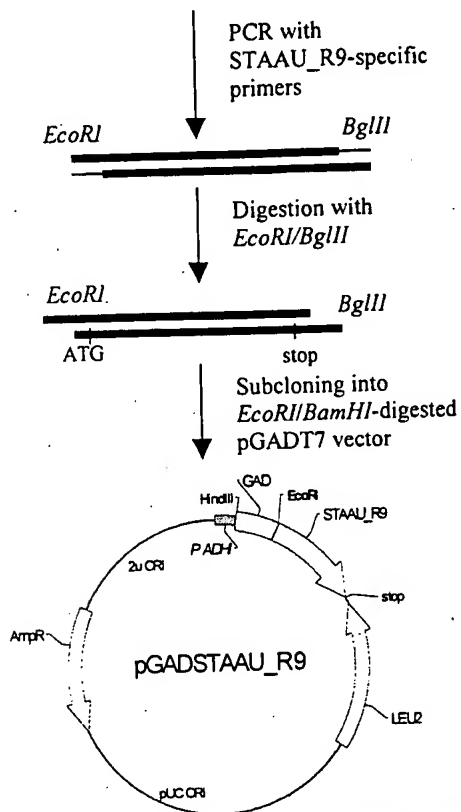
[illegible]

TEST"2225200T

seq1	413	VAPFFNVSPEQLANEIQF--NQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKAERAF	470
	:	: : :: : : :	
seq2	407	LRIYLR--QELGNKLGILDDSQLERLMPKAAESGVS RVP-----QLKRRTMRIL	454
seq1	471	LKHLMRDKD--TFLNYYESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNE	528
	:	::: : : :: :: : : :::	
seq2	455	IGLLVQNPELATLVPPLNLDENKLPGLG---LFREL VNTCLSQPGLTTGQLLEHYRGTN	511
seq1	529	LRETLISLEQY-----NLNDEPYENEIDDYVNVINEKGOETIESLNHKLREATR--IGD	580
	:	: : : : : : : : : :	
seq2	512	NAATLEKLSMWDDIADKNIAEQFTTDSLNMHMFDSLLELRQEELIA-----RERTHGLSNE	566
seq1	581	VELQYYLQQIVAKNKERM	599
	:	: : :	
seq2	567	ERLELWTLNQELAKK----	581

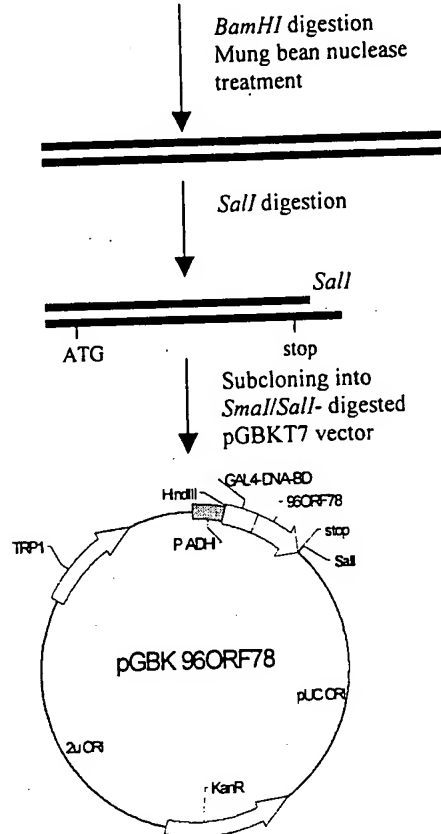
FIGURE 8

A- *Staphylococcus aureus* genomic DNA



B-

96pTMSMLacORF78



C-

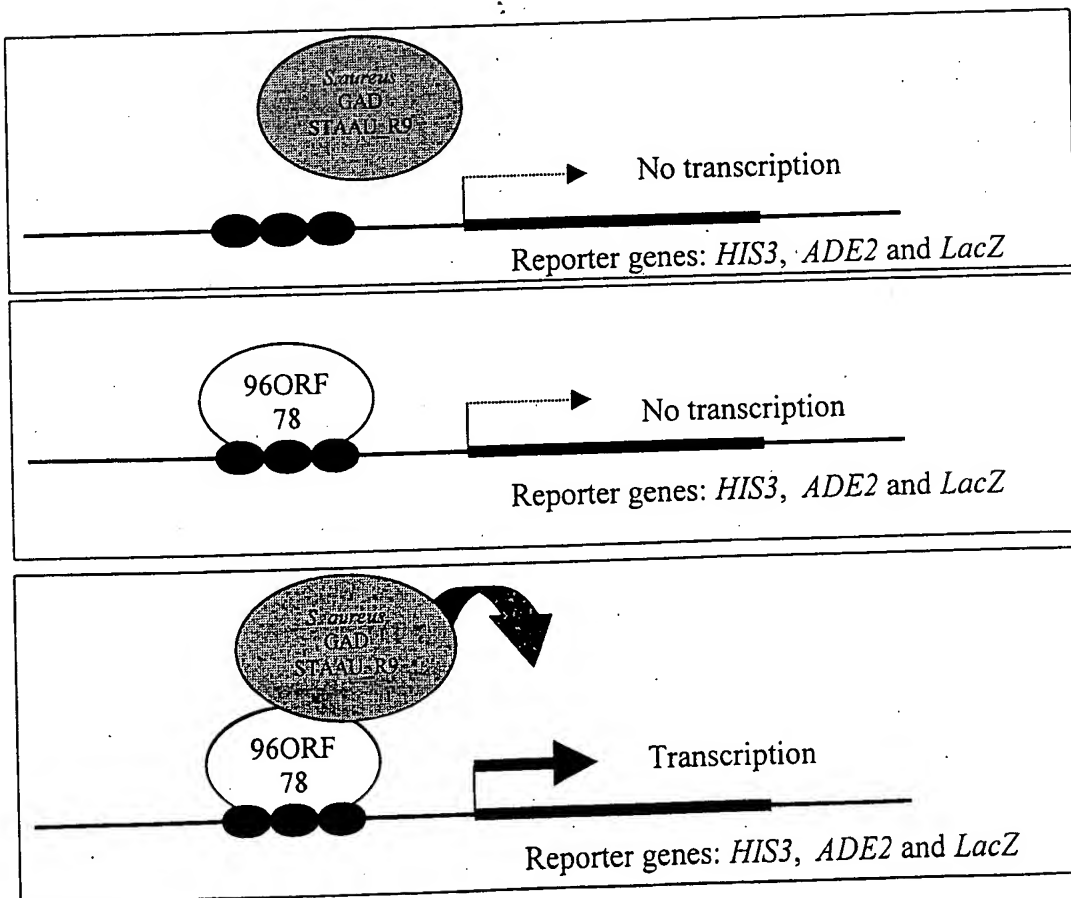
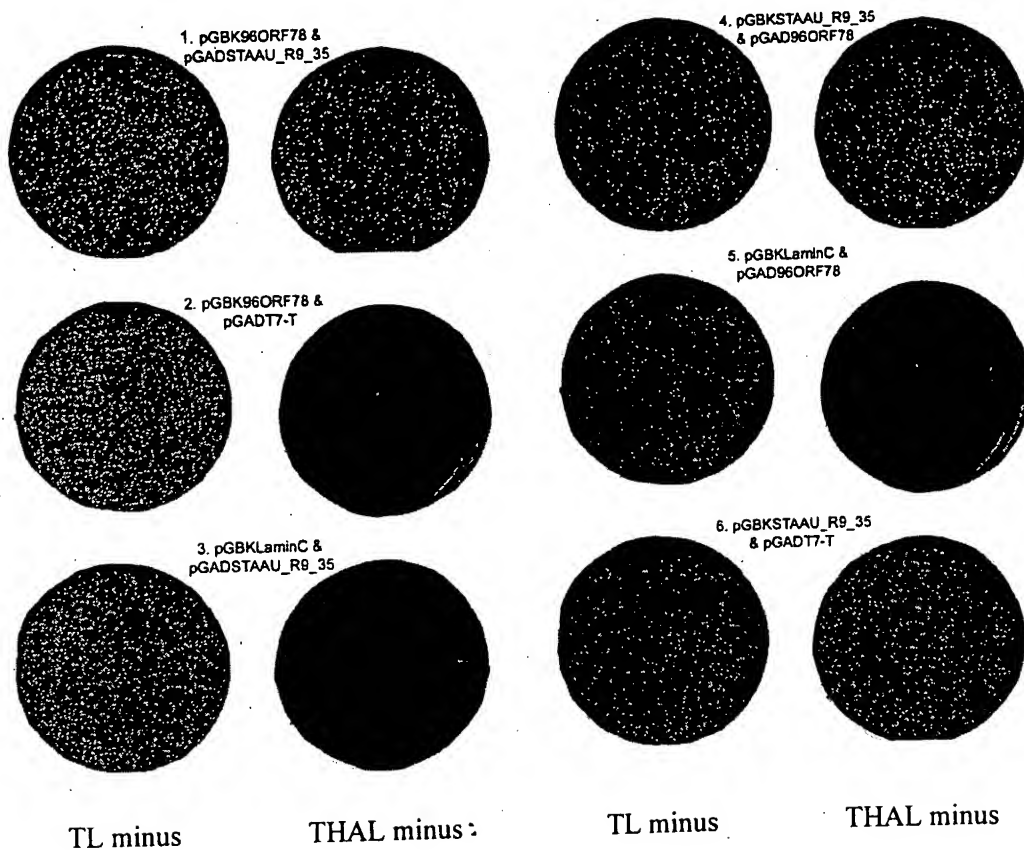
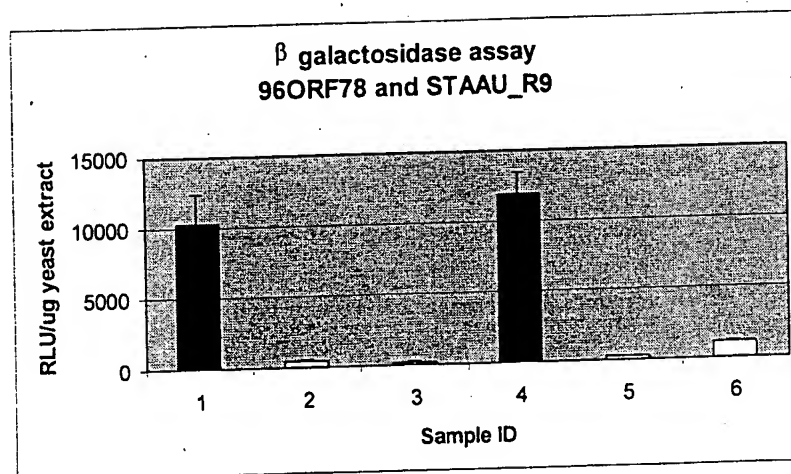


FIGURE 9

A.



B.



Sample	Yeast co-transformants		RLU (avg)	SD
	Plasmid 1	Plasmid 2		
1	pGBK 96ORF78	pGADSTAAU_R9_35	10,250	2,080
2	pGBK 96ORF78	pGADT7-T	475	38
3	pGBK Lamin C	pGADSTAAU_R9_35	224	10
4	pGBKSTAAU_R9_35	pGAD 96ORF78	11,935	1,477
5	pGBK Lamin C	pGAD 96ORF78	243	12
6	pGBKSTAAU_R9_35	pGADT7-T	1,121	37

FIGURE 10

A. Fragments of STAAU_R9

B.

Interaction with
96ORF78

1	599	Yes
35	599	Yes
35	342	No
229	402	No
229	599	Yes
380	599	Yes
380	449	No
380	490	No
380	530	No
380	561	No
449	599	Yes
490	599	Yes
530	599	Yes
561	599	Yes

GQETIESLNHKLREATRIGDVELQKYVYLQQIVAKNKERM

SEQ ID NO: 6 STAAU_R9_561-599
AMINO ACID SEQUENCE

SEQ ID NO: 5 STAAU_R9_1683-1800
NUCLEIC ACID SEQUENCE

GGACAAAGAAAACAATTGAGTCATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTA
GAATTACAAAAATACTATTACAGCAAAATTGTTGCTAAGAATAAAGAAGCATGTAG

C.

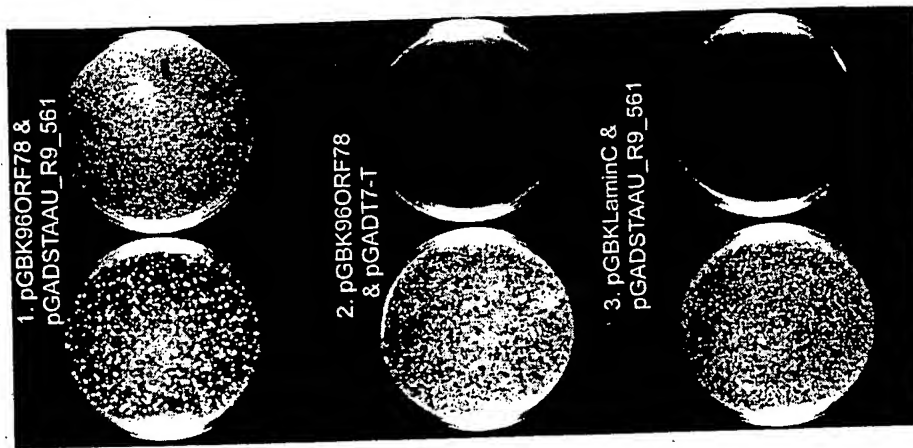


FIGURE 11

A.

	Primer name	Primer sequence 5' → 3'	Restriction site
SEQ ID NO: 8	R9_5E3	5'-ccggaattcTTGCGAATAGATCAATCG-3'	EcoRI
SEQ ID NO: 9	R9_3BG	5'-ggaagatctCTACATGCGTTCTTTATTTC-3'	BglII
SEQ ID NO: 10	R9_5E	5'-ccggaattcATGATAGGTTTGTCCT-3'	EcoRI
SEQ ID NO: 11	R9_5E1	5'-ccggaattcCCAAAATACCTAATAGTCC-3'	EcoRI
SEQ ID NO: 12	R9_5E2	5'-ccggaattcGCACATAATGACCTTTCA-3'	EcoRI
SEQ ID NO: 13	R9_342R	5'-cgcgatccATGCTGATGGCAATTG-3'	BamHI
SEQ ID NO: 14	R9_402R	5'-ccatcgatGATTTTCATAAGCGAAATATC-3'	Clal
SEQ ID NO: 15	R9_449F	5'-ccggaattcCCTGAGCCAATTGGTATGGC-3'	EcoRI
SEQ ID NO: 16	R9_449R	5'-cgcgatccctaAGGTTCAATGTAACCGCC-3'	BamHI
SEQ ID NO: 17	R9_490F	5'-ccggaattcAAGGATAACTTCACAAATCAG-3'	EcoRI
SEQ ID NO: 18	R9_490R	5'-cgcgatccctaCTTATCAACACTTTTCATAATA-3'	BamHI
SEQ ID NO: 19	R9_530F	5'-ccggaattcAGAGAAACACTAATTAGCTTA-3'	EcoRI
SEQ ID NO: 20	R9_530R	5'-cgcgatccctaTCTCAACTCATTGGAATTAAC-3'	BamHI
SEQ ID NO: 21	R9_561F	5'-ccggaattcGGACAAGAAACAATTGAGTC-3'	EcoRI
SEQ ID NO: 7	R9_561R	5'-cgcgatccctaTCCTTTTTCATTAATAACATTG-3'	BamHI

B.

Cloning of SEQ ID NO: 2 amino acid fragments	Sense primer	Antisense primer
1-599	R9_5E3	R9_3BG
35-599	R9_5E	R9_3BG
35-342	R9_5E	R9_342R
229-402	R9_5E1	R9_402R
229-599	R9_5E1	R9_3BG
380-599	R9_5E2	R9_3BG
380-449	R9_5E2	R9_449R
380-490	R9_5E2	R9_490R
380-530	R9_5E2	R9_530R
380-561	R9_5E2	R9_561R
449-599	R9_449F	R9_3BG
490-599	R9_490F	R9_3BG
530-599	R9_530F	R9_3BG
561-599	R9_561F	R9_3BG